

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: March 10, 2000, 17:37:18 ; Search time 904.17 Seconds

(Without alignments)
-6360.431 Million cell updates/sec

Title: US-09-126-945-1
Perfect score: 1894
Sequence: 1 gtcgactctctccagcagc.....ataagatctacagagctg 1894
Scoring table: IDENTITY,NUC
Searched: 82183 seqs, -151819014 residues
Database: GenEmbl:*
Word size: 0
Number of hits that pass the threshold: 1642386

1: gb_dal.*
2: gb_dal.*
3: gb_dal.*
4: gb_ov.*
5: gb_ov.*
6: gb_ov.*
7: gb_p11.*
8: gb_p12.*
9: gb_p12.*
10: gb_p12.*
11: gb_p13.*
12: gb_p13.*
13: gb_p13.*
14: gb_p13.*
15: gb_p13.*
16: gb_p13.*
17: gb_p13.*
18: gb_p13.*
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22: gb_p13.*
23: gb_p13.*
24: gb_p13.*
25: gb_p13.*
26: gb_p13.*
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32: gb_p13.*
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34: gb_p13.*
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37: gb_p13.*
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39: gb_p13.*
40: gb_p13.*
41: gb_p13.*
42: gb_p13.*
43: gb_p13.*
44: gb_p13.*
45: gb_p13.*
46: gb_p13.*
47: gb_p13.*
48: gb_p13.*
49: gb_p13.*

50: gb_p13.*
Prod No. is the number of results predicted by chance to have a
score greater than the observed score. The results are being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query	Length	DB	ID	Description
1	1894	100.0	1894	40	AF071538		AF071538 Homo sapi
2	751.2	39.7	1704	12	AB019436		AB019436 Mus muscu
3	150.8	8.0	352	13	DROE053A		MB8474 Drosophila
C	4	150.8	8.0	139371	41	AC008253	AC008253 Drosophila
5	150.8	8.0	38178	43	AC015374		AC015374 Drosophila
6	147.6	7.8	1832	35	AF106564		AF106564 Strongylo
C	7	147.6	7.8	137899	43	AC007818	AC007818 Drosophila
9	147.6	7.8	137899	43	AC007818		AC007818 Drosophila
10	99.2	5.2	12473	33	DROE053A		M17083 Drosophila
11	99.2	5.2	5315	34	DROE053A		X15087 Drosophila
12	97.6	5.2	115815	42	AC009371		AC009371 Drosophila
13	97.6	5.2	115815	42	AB016193		AB016193 Homo sapi
14	86.4	4.6	2695	9	H0000000		M25269 Homo sapien
15	86.4	4.6	2695	9	H0000000		AF075706 Gallus ga
16	84.4	4.5	948	4	AF075706		AF008072 Homo sapi
17	84.4	4.5	948	4	AF075706		AF075706 Gallus ga
18	83.6	4.4	2286	12	MMELK1P		AB02571 M. musculus
19	83.6	4.4	2286	12	MMELK1P		AB02571 M. musculus
20	83.4	4.4	1403	9	HS00NAFEV3		Y08979 H. sapiens F
21	83.4	4.4	1403	9	HS00NAFEV3		Y08979 H. sapiens F
22	82.8	4.4	1901	9	HS00NAFEV3		Y08979 H. sapiens F
23	82.8	4.4	1901	9	HS00NAFEV3		Y08979 H. sapiens F
24	82.8	4.4	1901	9	HS00NAFEV3		Y08979 H. sapiens F
25	81.4	4.3	3586	12	AF016714		AF016714 Mus muscu
26	79.8	4.2	1447	40	AF147782		AF147782 Mus muscu
27	78.4	4.1	2657	5	AR026645		AR026645 Sequence
28	78.4	4.1	2657	5	AR026645		AR026645 Sequence
29	78.4	4.1	2657	5	AR026645		AR026645 Sequence
30	78.4	4.1	2657	5	AR026645		AR026645 Sequence
31	78.2	4.1	1309	10	AF006070		AF006070 Homo myelo
32	78.2	4.1	1309	10	AF006070		AF006070 Homo myelo
33	78.2	4.1	1309	10	AF006070		AF006070 Homo myelo
34	78.2	4.1	1309	10	AF006070		AF006070 Homo myelo
35	78.2	4.1	1309	10	AF006070		AF006070 Homo myelo
36	78.2	4.1	1309	10	AF006070		AF006070 Homo myelo
37	78.2	4.1	1309	10	AF006070		AF006070 Homo myelo
38	78.2	4.1	1309	10	AF006070		AF006070 Homo myelo
39	78.2	4.1	1309	10	AF006070		AF006070 Homo myelo
40	78.2	4.1	1309	10	AF006070		AF006070 Homo myelo
41	78.2	4.1	1309	10	AF006070		AF006070 Homo myelo
42	78.2	4.1	1309	10	AF006070		AF006070 Homo myelo
43	78.2	4.1	1309	10	AF006070		AF006070 Homo myelo
44	78.2	4.1	1309	10	AF006070		AF006070 Homo myelo
45	78.2	4.1	1309	10	AF006070		AF006070 Homo myelo

ALIGNMENTS

RESULT 1
AF071538
LOCUS AF071538 1894 bp mRNA
DEFINITION Homo sapiens E15 transcrip factor PDEF (PDEF) mRNA, complete
ACCESSION AF071538
VERSION AF071538.1 GI:4007417
KEYWORDS
SOURCE human
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominoidea; Homo.

COMMENT

On Sep 24, 1999 this sequence version replaced g1:5902266. For further information about this sequence, including its location and relationship to other sequences, please visit our sequence database (<http://www.frlitility.org/Sequence/>) or send email to frlility@fsl.frlitility.org. In this submission meet the following cutoffs: length > 200 bases.

* NOTE: This is a 'working draft' sequence. It currently consists of 82 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N's, but the exact sizes of the gaps are unknown. This record is intended to be updated as more sequence is as soon as it is available and the accession number will be preserved.

1 572: contig of 572 bp in length
573 652: gap of unknown length
574 1462: contig of 510 bp in length
1163 1164: gap of unknown length
1164 1168: contig of 676 bp in length
1168 1199: gap of unknown length
1199 2664: contig of 655 bp in length
2664 3404: contig of 651 bp in length
3404 3485: gap of unknown length
3485 3594: contig of 430 bp in length
3594 4327: contig of 653 bp in length
4327 4358: gap of unknown length
4358 4738: contig of 686 bp in length
4738 5503: gap of unknown length
5503 6335: contig of 832 bp in length
6335 6415: gap of unknown length
6415 7796: contig of 981 bp in length
7796 7937: gap of unknown length
7937 8017: contig of 681 bp in length
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9339 9420: gap of unknown length
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10121 10201: gap of unknown length
10201 10761: contig of 560 bp in length
10761 10841: gap of unknown length
10841 11485: gap of unknown length
11485 11565: gap of unknown length
11565 12127: contig of 611 bp in length
12127 12256: gap of unknown length
12256 13142: contig of 886 bp in length
13142 13257: gap of unknown length
13257 13374: contig of 652 bp in length
13374 13874: gap of unknown length
13874 15187: gap of unknown length
15187 15198: gap of unknown length
15198 16333: gap of unknown length
16333 16976: contig of 743 bp in length
16976 17056: gap of unknown length
17056 18209: contig of 1153 bp in length
18209 19328: gap of unknown length
19328 19766: gap of unknown length
19766 21223: contig of 1378 bp in length
21223 21903: gap of unknown length
21903 22698: contig of 1315 bp in length
22698 22698: gap of unknown length
22698 24507: contig of 1359 bp in length
24507 24963: gap of unknown length
24963 25044: gap of unknown length
25044 26303: contig of 1239 bp in length
26303 27193: contig of 811 bp in length
27193 27273: gap of unknown length
27273 28205: contig of 932 bp in length

28205 28285: gap of unknown length
28285 29927: contig of 1642 bp in length
29927 31006: gap of unknown length
31006 31087: contig of 999 bp in length
31087 31968: gap of unknown length
31968 32075: gap of unknown length
32075 33298: contig of 1222 bp in length
33298 33377: gap of unknown length
33377 35041: contig of 1664 bp in length
35041 35122: gap of unknown length
35122 37263: contig of 1642 bp in length
37263 37998: gap of 655 bp in length
37998 38912: contig of 1334 bp in length
38912 38992: gap of unknown length
38992 40750: contig of 1758 bp in length
40750 40830: gap of unknown length
40830 42533: contig of 1823 bp in length
42533 44356: contig of 1623 bp in length
44356 44357: gap of unknown length
44357 46335: contig of 1899 bp in length
46335 46415: gap of unknown length
46415 47879: contig of 1464 bp in length
47879 47959: gap of unknown length
47959 48800: contig of 1801 bp in length
48800 49260: gap of unknown length
49260 51596: contig of 1736 bp in length
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51677 52715: contig of 1039 bp in length
52715 52795: gap of unknown length
52795 54355: contig of 1560 bp in length
54355 54435: gap of unknown length
54435 55252: contig of 1110 bp in length
55252 57376: contig of 1731 bp in length
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57457 60745: contig of 3289 bp in length
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60825 62405: contig of 1580 bp in length
62405 62485: gap of unknown length
62485 63339: gap of unknown length
63339 65968: contig of 2029 bp in length
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65969 68286: contig of 2238 bp in length
68286 68367: gap of unknown length
68367 70709: contig of 2343 bp in length
70709 70709: gap of unknown length
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72381 72902: gap of unknown length
72902 76176: contig of 3194 bp in length
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76555 79093: contig of 2838 bp in length
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83289 85034: contig of 1745 bp in length
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96718 101120: contig of 4402 bp in length
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22 CONA	520 d	448 c	379 g	477 t
GIN				

[illegible]

1024	1103	gap of unknown length	1023	contig of 103 bp in length	10034	gap of unknown length	9995	contig of 991 bp in length	9884	gap of unknown length	9864	gap of unknown length	9854	contig of 91 bp in length	9844	gap of unknown length	9834	contig of 666 bp in length	8828	gap of unknown length	8218	gap of unknown length	7921	gap of unknown length	7891	gap of unknown length	6991	contig of 939 bp in length	5972	gap of unknown length	5892	contig of 835 bp in length	5891	contig of 835 bp in length	5055	gap of unknown length	4977	gap of unknown length	4935	gap of unknown length	4875	gap of unknown length	4834	contig of 776 bp in length	3489	gap of unknown length	3409	gap of unknown length	2491	contig of 918 bp in length	2411	2490	gap of unknown length	2410	contig of 1307 bp in length	1104	2410	contig of 1307 bp in length	1024	1103	gap of unknown length
1024	1103	gap of unknown length	1023	contig of 103 bp in length	10034	gap of unknown length	9995	contig of 991 bp in length	9884	gap of unknown length	9864	gap of unknown length	9854	contig of 91 bp in length	9844	gap of unknown length	9834	contig of 666 bp in length	8828	gap of unknown length	8218	gap of unknown length	7921	gap of unknown length	7891	gap of unknown length	6991	contig of 939 bp in length	5972	gap of unknown length	5892	contig of 835 bp in length	5891	contig of 835 bp in length	5055	gap of unknown length	4977	gap of unknown length	4935	gap of unknown length	4875	gap of unknown length	4834	contig of 776 bp in length	3489	gap of unknown length	3409	gap of unknown length	2491	contig of 918 bp in length	2411	2490	gap of unknown length	2410	contig of 1307 bp in length	1104	2410	contig of 1307 bp in length	1024	1103	gap of unknown length

[illegible]

COMMENT

Laboratory, MS 64-121, Berkeley, CA 94720, USA
On Aug 2, 1999 this sequence version replaced gi:5649213.
Genetic information about this sequence, including its location
and relationship to other sequences, is available at the
archive web site (<http://www.ncbi.nlm.nih.gov/sequence/>) or send email
to hdg@fruitfly.berkeley.edu. All contigs in this submission meet
the following cutoffs: length >= 200 bases.

NOTE: This is a 'working draft' sequence. It currently
consists of 94 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Contigs are represented as
runs of 'N' but they are not necessarily adjacent.
This record will be updated with the finished sequence
as soon as it is available and the accession number will
be preserved.

1 847 846: contig of 846 bp in length
847 928: gap of unknown length
1520 1328: contig of 703 bp in length
1520 1328: gap of unknown length
11710 3034: gap of unknown length
3035 4305: contig of 1271 bp in length
4306 4385: gap of unknown length
4386 5408: contig of 1024 bp in length
5410 5485: gap of unknown length
5485 6587: contig of 1018 bp in length
6588 7425: contig of 838 bp in length
7426 7505: gap of unknown length
7506 8263: contig of 757 bp in length
8263 8343: gap of unknown length
8343 9210: contig of 868 bp in length
9211 9290: gap of unknown length
9291 10110: contig of 819 bp in length
10111 10647: contig of 537 bp in length
10648 10727: gap of unknown length
10728 11695: contig of 968 bp in length
11696 11775: gap of unknown length
11776 12463: contig of 688 bp in length
12464 13265: contig of 801 bp in length
13266 14623: contig of 1357 bp in length
13267 14703: gap of unknown length
14624 14703: gap of unknown length
14704 15407: contig of 704 bp in length
15408 15487: gap of unknown length
15488 16114: contig of 627 bp in length
16115 16194: gap of unknown length
16195 17231: contig of 1037 bp in length
17232 18351: contig of 920 bp in length
18352 18731: gap of unknown length
18732 19326: contig of 1095 bp in length
19327 19406: gap of unknown length
19407 20721: contig of 1315 bp in length
20722 20801: gap of unknown length
20802 22154: gap of unknown length
22155 23387: contig of 1193 bp in length
23388 23467: gap of unknown length
23468 24368: contig of 871 bp in length
24369 25754: gap of unknown length
25755 27378: gap of unknown length
27379 28093: contig of 635 bp in length
28094 28173: gap of unknown length
28174 29298: contig of 1325 bp in length
29299 30533: gap of unknown length
30534 30533: contig of 875 bp in length
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30534 31577: contig of 1044 bp in length
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31578 32537: contig of 1195 bp in length
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32934 34455: gap of unknown length
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34537 36322: contig of 1787 bp in length
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41024 41834: contig of 811 bp in length
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41915 43333: contig of 1319 bp in length
43334 43313: gap of unknown length
43314 43716: contig of 2445 bp in length
43717 44720: contig of 1932 bp in length
44721 47850: gap of unknown length
47851 49194: contig of 1344 bp in length
49195 49274: gap of unknown length
49275 50726: contig of 1452 bp in length
50727 50806: gap of unknown length
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52159 53703: contig of 1244 bp in length
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53784 55620: contig of 1837 bp in length
55621 55700: gap of unknown length
55701 57561: contig of 1861 bp in length
57562 57641: gap of unknown length
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61048 61127: gap of unknown length
61128 62765: contig of 1638 bp in length
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62846 65301: contig of 2436 bp in length
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65382 66563: gap of unknown length
66564 68942: contig of 2119 bp in length
68943 69022: gap of unknown length
69023 70711: contig of 1689 bp in length
70712 70791: gap of unknown length
70792 72773: contig of 1982 bp in length
72774 72853: gap of unknown length
72854 75751: gap of unknown length
75752 77675: contig of 1924 bp in length
77676 77755: gap of unknown length
77756 80248: contig of 2494 bp in length
80249 80329: gap of unknown length
80330 83371: contig of 3042 bp in length
83372 84341: gap of unknown length
84342 86524: gap of unknown length
86525 90786: contig of 4182 bp in length
90787 90866: gap of unknown length
90867 96542: contig of 5676 bp in length
96543 97268: gap of unknown length
97269 97726: contig of 604 bp in length
97727 98028: contig of 723 bp in length
98029 98109: gap of unknown length
98110 98868: contig of 759 bp in length
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[illegible]

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		1..66
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		/codon_start=-1
		/db_xref="GI:4126582"
		db_xref="GI:4126582"
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		755..1186
	exon	/gene=Elk1*
		179..238
	exon	/number=5
		179..238
	exon	/gene=Elk1*
		1289..2695
	exon	/number=6
		1289..2695
		/number=7
		1385..2695
BASE COUNT	3'UTR	541 a 811 c 721 g 622 t
ORIGIN		
Query Match		4.6% Score 86.4; Db 9; Length 2695;
Best Local Similarity		60.5%; Pred. No. 2; 2e-06;
Matches 179; Conservative 0; Mismatches 111; Indels 6; Gaps 2;		
Oy	1166 ctgtgcgaagtcctcagaagatgtagctaccacagccacagctatggcgctcaattagg	1235
Db	119 ctgtgcgaagtttgtctcactcctctctctctctctctctctctctctctctctctctct	175
Oy	1226 ttgtctcaacaaggagaaaggcatctctcaaatctgagaagatctcacgccagtgtgcgcgcgtc	1285
Db	117 ttgtctcaacaaggagaaaggcatctctcaaatctgagaagatctcacgccagtgtgcgcgcgtc	175
Oy	1286 ttgggtgatctcgcaagaagaaacggtccgcgcatactacccaagaagtcgtgacgctccatcgc	1345
Db	236 ttgggtgatctcgcaagaagaaacggtccgcgcatactacccaagaagtcgtgacgctccatcgc	235
Oy	1346 cagtatcagaagaaggagacatccagtgaaagcagagacatccagtcagcgcgcgtctcagc	1405
Db	2296 tttctacctatctaacaaagacatcccccaag--gtgacgcgcgcacgaattcccttcacaa	352
Oy	1406 ttctgtgaccccacatctgtgctcgtgcgcagaagccttgaaccgcgcctccacagggc	1461
Db	353 ttctgtgtcttacctatgagctgcagagctctcactcactgagacatccgccaccacgc	408
RESULT 14		
HOMELK1A		
LOCUS	HOMELK1A	2266 bp mRNA PRI 07-NOV-1994
DEFINITION	Homo sapiens tyrosine kinase (ELK1) oncogene mRNA, complete cds.	
VERSION	M23269.1 GI:5130208	
KEYWORDS	EST1 gene; oncogene; TYROSINE KINASE.	
SOURCE	Homo sapiens CDNA to mRNA.	
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;	

[illegible]

Db 1022 ATCAGGTGGATAGACAGACCAAGGTATCTTCAAGATCGAGGACTCTGTGAGGTGCC 1081

Query Match	7.8%;	Score 147.6;	DB 43;	Length 137899;
Best Local Similarity	72.2%;	Pred. No. 1.3e-17;		
Matches 192;	Conservative 0;	Mismatches 74;	Indels 0;	Gaps 0

	RESULT	8	
LOCUS	AC0068217		HTC
DEFINITION	Drosophila melanogaster chromosome 3 clone BACR10023 (Df(8) Rp ^r -1.0 J.3 mpB-98B strain y cn bw sp. *** SEQUENCING IN PROGRESS.		
ACCSSION	AC0068217.2	G15670464	
KEYWORDS	EST; HGS_PMSHEL		
SOURCE	Drosophila melanogaster		

TITLE Sequencing of *Drosophila melanogaster*

REFERENCES

Eukaryotes; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscophora; Ephyraeidae; Drosophilidae; Drosophila.

AUTHORS

Gelinkler S.R., Ashburner A., Archana T.T., Batzer F., Blazer R.G., Bult C.J., Chapple M., Claret J.C., Chew K.W., Clelland L.M., DeBenedictis G., Chapman M., Chamber C., Chey W., Cicciocioppo R., Butlerhoff C., Chappman M., Chavakis C., Chaw K.W., Cicciocioppo R., Doyle C.M., Farfan D.E., Galle R., George R.A., Harris N.U., Hoskins R.A., Houston K.A., Hummel S.R., Katri R., Kearney L., Kim E., Lee B., Lewis S., Li P., Lombard M.A., Maeda F., Mosher L.A., Mostoslavsky M., Nixon K., Pacheco J.M., Park S., Pfeiffer B., Poorn L., Seguelite A., Seihl H., Shat E., Smith R., Smith R.K., Wan K.H., Weinburg T., Zhang R., Zierlin L.L. and Rubin G.

JOURNAL
REFERENCES
AUTHORS

Unpublished
2 (bases 1 to 121935)
Rajalingam, S., Rajadurai, A., Arciniegua, T.T., Baxter, E., Blazek, R.G.,
Bautista, J., Bhat, S., Bhat, S., Bhat, S., Bhat, S., Bhat, S.,
Butterfield, R., Calkins, D.E., Callier, R.C., Chen, H., Ciesielski, L.,
Doyle, C.M., Farfan, D.B., Geller, R., Geller, R., Geller, R.,
Haskins, R.A., Housman, K., Hummel, S.R., Kariya, K., Kearney, L.,
Kim, E., Lee, B., Lewis, S., Li, P., Lomax, H.A., Mazza, P.,
Moshel, A.R., Moshel, M., Nixon, K., Poch, J.M., Park, S.,
Pfeiffer, B., Poon, L., Sequerra, A., Sethi, H., Smit, E.,
Srivastava, R., Wan, K.H., Weinburg, T., Zhang, R., Zierman, L.L., and
Rudin, G.M.

GenBank accession
Submitted (29-01-1991), Drosophila Genome Center, Lawrence Berkeley
Laboratory, MS 64-1121, Berkeley, CA 94720, USA

COMMENT

On Aug 2, 1999 this sequence about virus sequence, including its localities.
For further information about this sequence, including its localities,
and relationship to other sequences, please visit our sequence
archive web site (<http://www.fruitfly.org/sequence/>) or send email to
bugreport@berkeley.edu. All contigs in this submission meet
the following cutoffs: length >= 200 bases.
The following contigs are in this submission:
* consists of 9 contigs in this submission.
* It currently
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will

.. be preserved.
 1 846: contig of 846 bp in length
 847 847: contig of 847 bp in length
 927 1628: contig of 701 bp in length
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 3035 4305: contig of 1271 bp in length
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 10648 10727: gap of unknown length
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 98949 99550: contig of 602 bp in length
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 100539 100539: gap of unknown length
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 Best Local Similarity 54.68; Pred. No. 3.1e-15;

Matches 17; Conservative 0; Mismatches 143; Indels 0; Gaps 0;

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 Qy 1277 gcccgcgcgtgagc 1336
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 Db 23275 GCCTACCGGTGAGTCTCTCAAGAGTCTCTCAAGCCAGCCAGCTAGCGCG 23334
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 Qy 1337 tccattcgcgcgtatctacaaagagagcgcgcgcgcgcgcgcgcgcgcgcgcgc 1396
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 Qy 1397 gtctacacgctgctgacccacacacacacacacacacacacacacacacacac 1456
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 Db 23455 NNN 23469
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RESULT 9

LOCUS DROE74A 6479 bp mRNA INV 26-APR-1993
 DEFINITION Drosophila melanogaster E74A protein.
 VERSION M17082.1 GI:157307
 KEYWORDS DNA-binding protein; E74A protein, D.melanogaster (strain Canton S), cDNA to mRNA, and DNA.
 SOURCE Drosophila melanogaster
 ORGANISM Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscivora; Spindoptera; Drosophilidae; Drosophila.
 REFERENCE 1 (Jones K.C., Hummel C.S., Jones C.W., Karim F.D. and Hogness, D.S. The Drosophila 74EF early putative protein E74, a complex ecdysone-inducible gene that encodes two ets-related proteins Cell 61, 85-99 (1990))
 JOURNAL CELL 61, 85-99 (1990)
 MEDLINE 90199900
 COMMENT Draft entry and computer-readable sequence for (1) kindly submitted by C.S.Hummel, 10-SEP-1990.
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BASE COUNT 1879 a 1641 c 1481 g 1478 t
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Query Match 5.28: Score 99.2; DB 34; Length 6479;
 Best Local Similarity 64.58; Pred. No. 7.e-09;
 Matches 165; Conservative 0; Mismatches 88; Indels 3; Gaps 1;

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 Qy 1218 ttcattagcgcgtcaacaaagagagagcattcaattcgaagcattccagccagctg 1277
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 Db 4632 TCATCAAGTGAACGACGAGAAAGGCGCTTCAAGCTGTGACGACGACGCTGTG 4691
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 Qy 1278 cccgcgcgtgagc 1337
 |||||
 Db 4692 CCGCCTGTG6GCHTGCACGACGACGACGACGACGACGACGACGACGACG 4751
 |||||
 Qy 1338 ccatcgcgcgtatctacaaagagagcgcgcgcgcgcgcgcgcgcgcgcgcgc 1397
 |||||
 Db 4752 CGCTAGAGTACTACTACACCGCGCATCTGCGCAGAGGTGSA---TGCGACGCGCTGG 4808
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 Qy 1398 tctaccagcttcgtgca 1413
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 Db 4809 TCTACAGTCTGTGCGA 4824
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RESULT 10

LOCUS DROE74B 5315 bp mRNA INV 26-APR-1993
 DEFINITION Drosophila melanogaster E74B protein.
 VERSION M37083.1 GI:157309
 KEYWORDS E74B protein.
 SOURCE D.melanogaster (strain Canton S), cDNA to mRNA, and DNA.
 ORGANISM Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscivora; Spindoptera; Drosophilidae; Drosophila.
 REFERENCE 1 (Jones K.C., Hummel C.S., Jones C.W., Karim F.D. and Hogness, D.S. The Drosophila 74EF early putative protein E74, a complex ecdysone-inducible gene that encodes two ets-related proteins Cell 61, 85-99 (1990))
 JOURNAL CELL 61, 85-99 (1990)
 MEDLINE 90199900
 COMMENT Draft entry and computer-readable sequence for (1) kindly submitted by C.S.Hummel, 10-SEP-1990.
 FEATURES
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